

TherapheresisSeq Listing.txt
SEQUENCE LISTING

<110> Universitaet Stuttgart
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GRUNWALD, Ingo
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<120> RECOMBINANT POLYPEPTIDES OF THE MEMBERS OF THE TNF LIGAND FAMILY AND USE
THEREOF

<130> 040045-0358701

<140> 10/594,189
<141> 2006-09-25

<150> PCT/EP2005/003158
<151> 2005-03-24

<150> DE 102004014983.6-4
<151> 2004-03-26

<160> 41

<170> PatentIn version 3.3

<210> 1
<211> 8
<212> PRT
<213> Artificial Sequence Sequence

<220>
<223> Description of Artificial Sequence: Synthetic flag-tag peptide sequence

<400> 1

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 2
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide linker sequence

<400> 2

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide linker sequence

<400> 3

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Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 4
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Linker sequence

<400> 4
ggtggcggtt ctgggtggcg ttctgggtggc ggatcc 36

<210> 5
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Linker sequence

<400> 5
ggtggcggtt ctgggtggcg ttctgggtggc gttctggtg gcggatcc 48

<210> 6
<211> 84
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: scTNF Primer I

<400> 6
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gatgataacccg aagttaaacct gacc 84

<210> 7
<211> 97
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: scTNF Primer II

<400> 7
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cgccacccag agcgatgata ccgaagtaaa cctgacc 97

<210> 8
<211> 43
<212> DNA
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<220>

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<223> Description of Artificial Sequence: scTNF Primer III	
<400> 8 ccccgaattc ggatcctctt ctcgtacccc gtctgacaaa ccg	43
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<220>	
<223> Description of Artificial Sequence: scTNF Primer IV	
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<220>	
<223> Description of Artificial Sequence: scTNF Primer V	
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<210> 11 <211> 97 <212> DNA <213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: cys-scTNF Primer VI	
<400> 11 aattcattaa agaggagaaa ttaactatgg gagagctcat cgaaggtcgc tgcgccggtg gatctggtca tcatcatcac catcacggct cagacgg	60 97
<210> 12 <211> 97 <212> DNA <213> Artificial Sequence	
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<223> Description of Artificial Sequence: cys-scTNF Primer VII	
<400> 12 cgctccgtct gagccgtat ggtgatgatg atgaccagat ccaccggcgc agcgaccc gatgagctct cccatagtta atttctcctc tttaatg	60 97
<210> 13 <211> 100 <212> DNA <213> Artificial Sequence	

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<220> Description of Artificial Sequence: Primer FasL#1R

<400> 13
atcgatttct agaccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60
cgccaccgag cttatataag ccgaaaaacg tctgagattc 100

<210> 14
<211> 35
<212> DNA
<213> Artificial Sequence

<220> Description of Artificial Sequence: Primer FasL#2F

<400> 14
ggggtagcgg ccgcgtgtc gacgattaca aagac 35

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220> Description of Artificial Sequence: Primer FasL#3F

<400> 15
agaaaaaaag gagctgagga aagtgg 26

<210> 16
<211> 36
<212> DNA
<213> Artificial Sequence

<220> Description of Artificial Sequence: Primer FasL#4F

<400> 16
ggggcggatc cgaaaaaaag gagctgagga aagtgg 36

<210> 17
<211> 50
<212> DNA
<213> Artificial Sequence

<220> Description of Artificial Sequence: Primer FasL#5R

<400> 17
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<210> 18
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: Primer HA-IF

<400> 18
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<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer HA-IIR

<400> 19
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<210> 20
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer TRAIL#1R

<400> 20
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cgccaccgcc aactaaaaag gccccgaaaa aactggcttc atggc 106

<210> 21
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer TRAIL#2F

<400> 21
gggtagaaat tcggaacctc tgagggaaacc atttctacag ttcaag 46

<210> 22
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer TRAIL#3F

<400> 22
aacctctgag gaaaccattt ctacag 26

<210> 23
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer TRAIL#4F

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<400> 23		
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<210> 24		
<211> 53		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Primer TRAIL#5R		
<400> 24		
ggggcctcta gaatcgatgg tcagccact aaaaaggccc cgaaaaaact ggc		53
<210> 25		
<211> 1506		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: scTNF-L short chain		
<220>		
<221> CDS		
<222> (1)..(1503)		
<400> 25		
atg aga gga tcg cat cac cat cac cat cac gga tca gcg tcg tct tct		48
Met Arg Gly Ser His His His His His Gly Ser Ala Ser Ser Ser		
1 5 10 15		
tct cgt acc ccg tct gac aaa ccg gtt gct cac gtt gtt gca aac ccg		96
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro		
20 25 30		
cag gct gaa ggt caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg		144
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu		
35 40 45		
ctg gct aac ggt gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct		192
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser		
50 55 60		
gaa ggc ctg tac ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc		240
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly		
65 70 75 80		
tgc ccg tcc acc cac gtt ctg ctg acc cac acc atc tct cgt atc gct		288
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala		
85 90 95		
gtt tcc tac cag acc aaa gta aac ctg ctg tct gca atc aaa tct ccg		336
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro		
100 105 110		
tgc cag cgt gaa acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa		384
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu		
115 120 125		

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ccg atc tac ctg ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu 130 135 140	432
tct gca gaa att aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly 145 150 155 160	480
cag gtt tac ttc ggt atc atc gct ctg ggt ggc ggt tct ggt ggc ggt Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Gly 165 170 175	528
tct ggt ggc gga tcc tct cgt acc ccg tct gac aaa ccg gtt gct Ser Gly Gly Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala 180 185 190	576
cac gtt gtt gca aac ccg cag gct gaa ggt caa ctg caa tgg ctg aac His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn 195 200 205	624
cgt cgt gct aac gct ctg ctg gct aac ggt gtt gaa ctg cgt gac aac Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn 210 215 220	672
cag ctg gtt gtt ccg tct gaa ggc ctg tac ctg atc tac tcc cag gtt Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val 225 230 235 240	720
ctg ttc aaa ggc cag ggc tgc ccg tcc acc cac gtt ctg ctg acc cac Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His 245 250 255	768
acc atc tct cgt atc gct gtt tcc tac cag acc aaa gta aac ctg ctg Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu 260 265 270	816
tct gca atc aaa tct ccg tgc cag cgt gaa acc ccg gaa ggt gct gaa Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu 275 280 285	864
gct aaa ccg tgg tac gaa ccg atc tac ctg ggt ggc gtt ttt caa ctg Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu 290 295 300	912
gag aaa ggt gac cgt ctg tct gca gaa att aac cgt ccg gac tac ctg Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu 305 310 315 320	960
gac ttc gca gaa tct ggt cag gtt tac ttc ggt atc atc gct ctg ggt Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly 325 330 335	1008
ggc ggt tct ggt ggc ggt tct ggt ggc gga tcc tct tct cgt acc ccg Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Arg Thr Pro 340 345 350	1056
tct gac aaa ccg gtt gct cac gtt gca aac ccg cag gct gaa ggt Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly 355 360 365	1104
caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly 370 375 380	1152

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gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr 385 390 395 400	1200
ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr 405 410 415	1248
cac gtt ctg ctg acc cac acc atc tct cgt atc gct gtt tcc tac cag His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln 420 425 430	1296
acc aaa gta aac ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu 435 440 445	1344
acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu 450 455 460	1392
ggg ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg tct gca gaa att Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile 465 470 475 480	1440
aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe 485 490 495	1488
ggg atc atc gct ctg tga Gly Ile Ile Ala Leu 500	1506

<210> 26
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTNF-L short chain peptide
<400> 26

Met Arg Gly Ser His His His His His Gly Ser Ala Ser Ser Ser
1 5 10 15

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
20 25 30

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
35 40 45

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
50 55 60

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
65 70 75 80

TherapheresisSeq Listing.txt

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
85 90 95

val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
100 105 110

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
115 120 125

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
130 135 140

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
145 150 155 160

Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Gly
165 170 175

Ser Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala
180 185 190

His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn
195 200 205

Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn
210 215 220

Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val
225 230 235 240

Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His
245 250 255

Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu
260 265 270

Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu
275 280 285

Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu
290 295 300

Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu
305 310 315 320

Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly
325 330 335

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Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Arg Thr Pro
340 345 350

Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly
355 360 365

Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
370 375 380

Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
385 390 395 400

Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
405 410 415

His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
420 425 430

Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
435 440 445

Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
450 455 460

Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
465 470 475 480

Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
485 490 495

Gly Ile Ile Ala Leu
500

<210> 27

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cys-sCTNF-L short chain

<220>

<221> CDS

<222> (1)..(1539)

<400> 27

atg gga gag ctc atc gaa ggt cgc tgc gcc ggt gga tct ggt cat cat
Met Gly Glu Leu Ile Glu Gly Arg Cys Ala Gly Gly Ser Gly His His
1 5 10 15

48

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cat cac cat cac ggc tca gac gga gcg tcg tct tct tct cgt acc ccg His His His His Gly Ser Asp Gly Ala Ser Ser Ser Ser Arg Thr Pro 20 25 30	96
tct gac aaa ccg gtt gct cac gtt gca aac ccg cag gct gaa ggt Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly 35 40 45	144
caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly 50 55 60	192
gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr 65 70 75 80	240
ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr 85 90 95	288
cac gtt ctg ctg acc cac acc atc tct cgt atc gct gtt tcc tac cag His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln 100 105 110	336
acc aaa gta aac ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu 115 120 125	384
acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu 130 135 140	432
ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg tct gca gaa att Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile 145 150 155 160	480
aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe 165 170 175	528
ggt atc atc gct ctg ggt gac ggt tct ggt gac ggt tct ggt gac gga Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly 180 185 190	576
tcc tct tct cgt acc ccg tct gac aaa ccg gtt gct cac gtt gtt gca Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala 195 200 205	624
aac ccg cag gct gaa ggt caa ctg caa tgg ctg aac cgt cgt gct aac Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn 210 215 220	672
gct ctg ctg gct aac ggt gtt gaa ctg cgt gac aac cag ctg gtt gtt Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val 225 230 235 240	720
ccg tct gaa ggc ctg tac ctg atc tac tcc cag gtt ctg ttc aaa ggc Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly 245 250 255	768
cag ggc tgc ccg tcc acc cac gtt ctg ctg acc cac acc atc tct cgt Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg	816

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260	265	270	
atc gct gtt tcc tac cag acc aaa gta aac ctg ctg tct gca atc aaa Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys 275	280	285	864
tct ccg tgc cag cgt gaa acc ccg gaa ggt gct gaa gct aaa ccg tgg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp 290	295	300	912
tac gaa ccg atc tac ctg ggt ggc gtt ttt caa ctg gag aaa ggt gac Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp 305	310	315	960
cgt ctg tct gca gaa att aac cgt ccg gac tac ctg gac ttc gca gaa Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu 325	330	335	1008
tct ggt cag gtt tac ttc ggt atc atc gct ctg ggt ggc ggt tct ggt Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly 340	345	350	1056
ggc ggt tct ggt ggc gga tcc tct tct cgt acc ccg tct gac aaa ccg Gly Gly Ser Gly Gly Ser Ser Arg Thr Pro Ser Asp Lys Pro 355	360	365	1104
gtt gct cac gtt gtt gca aac ccg cag gct gaa ggt caa ctg caa tgg Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp 370	375	380	1152
ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt gtt gaa ctg cgt Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg 385	390	395	1200
gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac ctg atc tac tcc Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser 405	410	415	1248
cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc cac gtt ctg ctg Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu 420	425	430	1296
acc cac acc atc tct cgt atc gct gtt tcc tac cag acc aaa gta aac Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn 435	440	445	1344
ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa acc ccg gaa ggt Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly 450	455	460	1392
gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg ggt ggc gtt ttt Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe 465	470	475	1440
caa ctg gag aaa ggt gac cgt ctg tct gca gaa att aac cgt ccg gac Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp 485	490	495	1488
tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc ggt atc atc gct Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala 500	505	510	1536
ctg tga			1542

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Leu

<210> 28
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cys-scTNF-L short peptide

<400> 28

Met Gly Glu Leu Ile Glu Gly Arg Cys Ala Gly Gly Ser Gly His His
1 5 10 15

His His His His Gly Ser Asp Gly Ala Ser Ser Ser Ser Arg Thr Pro
20 25 30

Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly
35 40 45

Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
50 55 60

Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
65 70 75 80

Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
85 90 95

His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
100 105 110

Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
115 120 125

Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
130 135 140

Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
145 150 155 160

Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
165 170 175

Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Ser Gly Gly Gly
180 185 190

Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala
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195 200 205

Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn
210 215 220

Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val
225 230 235 240

Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly
245 250 255

Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg
260 265 270

Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys
275 280 285

Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp
290 295 300

Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
305 310 315 320

Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu
325 330 335

Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly
340 345 350

Gly Gly Ser Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro
355 360 365

Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp
370 375 380

Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg
385 390 395 400

Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
405 410 415

Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu
420 425 430

Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn
435 440 445

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Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly
450 455 460

Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe
465 470 475 480

Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp
485 490 495

Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala
500 505 510

Leu

<210> 29
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scFasL sequence

<220>
<221> CDS
<222> (1)..(1473)

<400> 29
atg gct atc atc tac ctc atc ctc ctg ttc acc gct gtg cg₇ ggc gc₈
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala 48
1 5 10 15

gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc acg cgt gaa aaa
 Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Thr Arg Glu Lys
 20 25 30

aag gag ctg agg aaa gtg gcc cat tta aca ggc aag tcc aac tca agg 144
Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg
35 40 45

tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc ctg ctt tct 192
Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser
50 55 60

gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa act ggg ctg
 Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu
 65 70 75 80

tac ttt gta tat tcc aaa gta tac ttc cg_g ggt caa tct tgc aac aac
Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn
85 90 95 288

ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag tat ccc cag 336
 Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln
 100 105 110

gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc act act ggg 384
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TherapheresisSeq Listing.txt

Theoretical Seq Listing.txt															
Asp	Leu	Val	Met	Met	Glu	Gly	Lys	Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly
115					120							125			
cag	atg	tgg	gcc	cgc	agc	agc	tac	ctg	ggg	gca	gtg	ttc	aat	ctt	acc
Gln	Met	Trp	Ala	Arg	Ser	Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr
130					135						140				432
agt	gct	gat	cat	tta	tat	gtc	aac	gta	tct	gag	ctc	tct	ctg	gtc	aat
Ser	Ala	Asp	His	Leu	Tyr	Val	Asn	Val	Ser	Glu	Leu	Ser	Leu	Val	Asn
145				150					155				160		480
ttt	gag	gaa	tct	cag	acg	ttt	ttc	ggc	tta	tat	aag	ctc	ggt	ggc	ggt
Phe	Glu	Glu	Ser	Gln	Thr	Phe	Phe	Gly	Leu	Tyr	Lys	Leu	Gly	Gly	Gly
					165				170				175		528
tct	ggt	ggc	ggt	tct	ggt	ggc	ggt	tct	ggt	ggc	gga	tca	gaa	aaa	aag
Ser	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Lys	Lys	Lys
			180				185					190			576
gag	ctg	agg	aaa	gtg	gcc	cat	tta	aca	ggc	aag	tcc	aac	tca	agg	tcc
Glu	Leu	Arg	Lys	Val	Ala	His	Leu	Thr	Gly	Lys	Ser	Asn	Ser	Arg	Ser
			195				200					205			624
atg	cct	ctg	gaa	tgg	gaa	gac	acc	tat	gga	att	gtc	ctg	ctt	tct	gga
Met	Pro	Leu	Glu	Trp	Glu	Asp	Thr	Tyr	Gly	Ile	Val	Leu	Leu	Ser	Gly
				210		215					220				672
gtg	aag	tat	aag	aag	ggt	ggc	ctt	gtg	atc	aat	gaa	act	ggg	ctg	tac
Val	Lys	Tyr	Lys	Lys	Gly	Gly	Leu	Val	Ile	Asn	Glu	Thr	Gly	Leu	Tyr
				225		230				235			240		720
ttt	gta	tat	tcc	aaa	gta	tac	ttc	cgg	ggt	caa	tct	tgc	aac	aac	ctg
Phe	Val	Tyr	Ser	Lys	Val	Tyr	Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Leu
				245			250					255			768
ccc	ctg	agc	cac	aag	gtc	tac	atg	agg	aac	tct	aag	tat	ccc	cag	gat
Pro	Leu	Ser	His	Lys	Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln	Asp
				260			265					270			816
ctg	gtg	atg	atg	gag	ggg	aag	atg	atg	agc	tac	tgc	act	act	ggg	cag
Leu	Val	Met	Met	Glu	Gly	Lys	Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly	Gln
			275			280					285				864
atg	tgg	gcc	cgc	agc	agc	tac	ctg	ggg	gca	gtg	ttc	aat	ctt	acc	agt
Met	Trp	Ala	Arg	Ser	Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser
				290		295				300					912
gct	gat	cat	tta	tat	gtc	aac	gta	tct	gag	ctc	tct	ctg	gtc	aat	ttt
Ala	Asp	His	Leu	Tyr	Val	Asn	Val	Ser	Glu	Leu	Ser	Leu	Val	Asn	Phe
				305		310				315			320		960
gag	gaa	tct	cag	acg	ttt	ttc	ggc	tta	tat	aag	ctc	ggt	ggc	ggt	tct
Glu	Glu	Ser	Gln	Thr	Phe	Phe	Gly	Leu	Tyr	Lys	Leu	Gly	Gly	Gly	Ser
				325			330					335			1008
ggt	ggc	ggt	tct	ggt	ggc	ggt	tct	ggt	ggc	gga	tcc	gaa	aaa	aag	gag
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Lys	Lys	Glu
			340			345					350				1056
ctg	agg	aaa	gtg	gcc	cat	tta	aca	ggc	aag	tcc	aac	tca	agg	tcc	atg
Leu	Arg	Lys	Val	Ala	His	Leu	Thr	Gly	Lys	Ser	Asn	Ser	Arg	Ser	Met
			355			360					365				1104

TherapheresisSeq Listing.txt

cct ctg gaa tgg gaa gac acc tat gga att gtc	ctg ctt tct gga gtg	1152	
Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val	Leu Leu Ser Gly Val		
370	375	380	
aag tat aag aag ggt ggc ctt gtg atc aat gaa	act ggg ctg tac ttt	1200	
Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu	Thr Gly Leu Tyr Phe		
385	390	395	400
gta tat tcc aaa gta tac ttc cgg ggt caa tct tgc	aac aac ctg ccc	1248	
Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys	Asn Asn Leu Pro		
405	410	415	
ctg agc cac aag gtc tac atg agg aac tct aag tat	ccc cag gat ctg	1296	
Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr	Pro Gln Asp Leu		
420	425	430	
gtg atg atg gag ggg aag atg atg agc tac tgc act	act act ggg cag atg	1344	
Val Met Met Glu Gly Lys Met Ser Tyr Cys Thr	Gly Gln Met		
435	440	445	
tgg gcc cgc agc agc tac ctg ggg gca gtg ttc	aat ctt acc agt gct	1392	
Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe	Asn Leu Thr Ser Ala		
450	455	460	
gat cat tta tat gtc aac gta tct gag ctc tct	ctg gtc aat ttt gag	1440	
Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser	Leu Val Asn Phe Glu		
465	470	475	480
gaa tct cag acg ttt ttc ggc tta tat aag ctc tga		1476	
Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu			
485	490		

<210> 30
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scFasL peptide sequence
<400> 30

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala
1 5 10 15

Ala Ala Asp Tyr Lys Asp Asp Asp Lys Glu Phe Thr Arg Glu Lys
20 25 30

Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg
35 40 45

Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser
50 55 60

Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu
65 70 75 80

TherapheresisSeq Listing.txt

Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn
85 90 95

Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln
100 105 110

Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly
115 120 125

Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
130 135 140

Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn
145 150 155 160

Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly Gly
165 170 175

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Lys Lys
180 185 190

Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser
195 200 205

Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly
210 215 220

Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr
225 230 235 240

Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu
245 250 255

Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp
260 265 270

Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln
275 280 285

Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser
290 295 300

Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe
305 310 315 320

Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly Gly Ser
325 330 335

TherapheresisSeq Listing.txt

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Glu Lys Lys Glu
340 345 350

Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met
355 360 365

Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val
370 375 380

Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe
385 390 395 400

Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro
405 410 415

Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
420 425 430

Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met
435 440 445

Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala
450 455 460

Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu
465 470 475 480

Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
485 490

<210> 31

<211> 1869

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: scTRAIL sequence

<220>

<221> CDS

<222> (1)..(1866)

<400> 31

atg gct atc atc tac ctc atc ctc ctg ttc acc gct gtg cggtt ggc gcg
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala
1 5 10 15

48

gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc gga acc tct gag
Ala Ala Asp Tyr Lys Asp Asp Asp Lys Glu Phe Gly Thr Ser Glu
20 25 30

96

gaa acc att tct aca gtt caa gaa aag caa caa aat att tct ccc cta

144

TherapheresisSeq Listing.txt

Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu
35					40							45			

gtg	aga	gaa	aga	ggt	cct	cag	aga	gta	gca	gct	cac	ata	act	ggg	acc	192
Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	
50					55						60					
aga	gga	aga	agc	aac	aca	ttg	tct	tcc	cca	aac	tcc	aag	aat	gaa	aag	240
Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	
65					70					75				80		
gct	ctg	ggc	cgc	aaa	ata	aac	tcc	tgg	gaa	tca	tca	agg	agt	ggg	cat	288
Ala	Leu	Gly	Arg	Lys	Ile	Ash	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	
									85		90			95		
tca	ttc	ctg	agc	aac	ttg	cac	ttg	agg	aat	ggt	gaa	ctg	gtc	atc	cat	336
Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	His	
						100		105				110				
gaa	aaa	ggg	ttt	tac	tac	atc	tat	tcc	caa	aca	tac	ttt	cga	ttt	cag	384
Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	
						115		120				125				
gag	gaa	ata	aaa	gaa	aac	aca	aag	aac	gac	aaa	caa	atg	gtc	caa	tat	432
Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	
						130		135			140					
att	tac	aaa	tac	aca	agt	tat	cct	gac	cct	ata	ttg	ttg	atg	aaa	agt	480
Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	Ser	
						145		150			155			160		
gct	aga	aat	agt	tgt	tgg	tct	aaa	gat	gca	gaa	tat	gga	ctc	tat	tcc	528
Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	
						165		170				175				
atc	tat	caa	ggg	gga	ata	ttt	gag	ctt	aag	gaa	aat	gac	aga	att	ttt	576
Ile	Tyr	Gln	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe		
						180		185			190					
gtt	tct	gta	aca	aat	gag	cac	ttg	ata	gac	atg	gac	cat	gaa	gcc	agt	624
Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala	Ser	
						195		200			205					
ttt	ttc	ggg	gcc	ttt	tta	gtt	ggc	ggt	ggc	ggt	tct	ggt	ggc	ggt	tct	672
Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
						210		215			220					
ggt	ggc	ggt	tct	ggt	ggc	gga	tca	acc	tct	gag	gaa	acc	att	tct	aca	720
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Thr	Ser	Glu	Glu	Thr	Ile	Ser	Thr	
						225		230			235			240		
gtt	caa	gaa	aag	caa	caa	aat	att	tct	ccc	cta	gtg	aga	gaa	aga	ggt	768
Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu	Val	Arg	Glu	Arg	Gly	
							245			250			255			
cct	cag	aga	gta	gca	gct	cac	ata	act	ggg	acc	aga	gga	aga	agc	aac	816
Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	
							260		265			270				
aca	ttg	tct	tct	cca	aac	tcc	aag	aat	gaa	aag	gct	ctg	ggc	cgc	aaa	864
Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	
							275		280			285				

TherapheresisSeq Listing.txt

ata aac tcc tgg gaa tca tca agg agt ggg cat tca ttc ctg agc aac Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn 290 295 300	912
ttg cac ttg agg aat ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr 305 310 315 320	960
tac atc tat tcc caa aca tac ttt cga ttt cag gag gaa ata aaa gaa Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu 325 330 335	1008
aac aca aag aac gac aaa caa atg gtc caa tat att tac aaa tac aca Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr 340 345 350	1056
agt tat cct gac cct ata ttg ttg atg aaa agt gct aga aat agt tgt Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys 355 360 365	1104
tgg tct aaa gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly 370 375 380	1152
ata ttt gag ctt aag gaa aat gac aga att ttt gtt tct gta aca aat Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn 385 390 395 400	1200
gag cac ttg ata gac atg gac cat gaa gcc agt ttt ttc ggg gcc ttt Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe 405 410 415	1248
tta gtt ggc ggt ggc ggt tct ggt ggc ggt tct ggt ggc ggt tct ggt Leu Val Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly 420 425 430	1296
ggc gga tcc acc tct gag gaa acc att tct aca gtt caa gaa aag caa Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln 435 440 445	1344
caa aat att tct ccc cta gtg aga gaa aga ggt cct cag aga gta gca Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala 450 455 460	1392
gct cac ata act ggg acc aga gga aga agc aac aca ttg tct tct cca Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro 465 470 475 480	1440
aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu 485 490 495	1488
tca tca agg agt ggg cat tca ttc ctg agc aac ttg cac ttg agg aat Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn 500 505 510	1536
ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc tat tcc caa Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln 515 520 525	1584
aca tac ttt cga ttt cag gag gaa ata aaa gaa aac aca aag aac gac Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp 530 535 540	1632

TherapheresisSeq Listing.txt

aaa caa atg gtc caa tat att tac aaa tac aca agt tat cct gac cct Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro 545 550 555 560	1680
ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct aaa gat gca Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala 565 570 575	1728
gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt gag ctt aag Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys 580 585 590	1776
gaa aat gac aga att ttt gtt tct gta aca aat gag cac ttg ata gac Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp 595 600 605	1824
atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc tga Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly 610 615 620	1869

<210> 32
<211> 622
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTRAIL peptide sequence

<400> 32

Met Ala Ile Ile Tyr Leu Ile Leu Phe Thr Ala Val Arg Gly Ala
1 5 10 15

Ala Ala Asp Tyr Lys Asp Asp Asp Lys Glu Phe Gly Thr Ser Glu
20 25 30

Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu
35 40 45

Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr
50 55 60

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
65 70 75 80

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
85 90 95

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
100 105 110

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
115 120 125

TherapheresisSeq Listing.txt

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
130 135 140

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
145 150 155 160

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
165 170 175

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
180 185 190

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
195 200 205

Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Ser Gly Gly Ser
210 215 220

Gly Gly Gly Ser Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr
225 230 235 240

Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly
245 250 255

Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
260 265 270

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
275 280 285

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
290 295 300

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
305 310 315 320

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
325 330 335

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
340 345 350

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
355 360 365

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
370 375 380

TherapheresisSeq Listing.txt

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
385 390 395 400

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
405 410 415

Leu Val Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
420 425 430

Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln
435 440 445

Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala
450 455 460

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
465 470 475 480

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
485 490 495

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
500 505 510

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
515 520 525

Thr Tyr Phe Arg Phe Gln Glu Ile Lys Glu Asn Thr Lys Asn Asp
530 535 540

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
545 550 555 560

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
565 570 575

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
580 585 590

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
595 600 605

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
610 615 620

TherapheresisSeq Listing.txt

<211> 1581

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scTNF sequence

<220>

<221> CDS

<222> (1)..(1578)

<400> 33

atg gct atc atc tac ctc atc ctc ctg ttc acc gct gtg cg	ggc gcg	48
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Met Ala Ile Ile Tyr Leu Ile Leu Phe Thr Ala Val Arg Gly Ala		
---	--	--

1	5	10	15
---	---	----	----

gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc gga tca tct tct		96
---	--	----

Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly Ser Ser Ser		
---	--	--

20	25	30
----	----	----

cga acc ccg agt gac aag cct gta gcc cat gtt gta gca aac cct caa		144
---	--	-----

Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln		
---	--	--

35	40	45
----	----	----

gct gag ggg cag ctc cag tgg ctg aac cgc cg	gcc aat gcc ctc ctg	192
--	---------------------	-----

Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu		
---	--	--

50	55	60
----	----	----

gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca gag		240
---	--	-----

Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu		
---	--	--

65	70	75	80
----	----	----	----

ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc tgc		288
---	--	-----

Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys		
---	--	--

85	90	95
----	----	----

ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc gtc		336
---	--	-----

Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val		
---	--	--

100	105	110
-----	-----	-----

tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc tgc		384
---	--	-----

Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys		
---	--	--

115	120	125
-----	-----	-----

cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag ccc		432
---	--	-----

Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro		
---	--	--

130	135	140
-----	-----	-----

atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc agc		480
---	--	-----

Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser		
---	--	--

145	150	155	160
-----	-----	-----	-----

gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg cag		528
---	--	-----

Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln		
---	--	--

165	170	175
-----	-----	-----

gtc tac ttt ggg atc att gcc ctg ggt ggc ggt tct ggt ggc ggt tct		576
---	--	-----

Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Ser Gly		
---	--	--

180	185	190
-----	-----	-----

ggt ggc ggt tct ggt ggc gga tca tca tct tct cga acc ccg agt gac		624
---	--	-----

Gly Gly Ser Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp		
---	--	--

TherapheresisSeq Listing.txt

195	200	205	
aag cct gta gcc cat gtt gta	gca aac cct caa gct gag ggg cag ctc		672
Lys Pro Val Ala His Val Val	Ala Asn Pro Gln Ala Glu Gly Gln Leu		
210	215	220	
cag tgg ctg aac cgc cg	gcc aat gcc ctc ctg gcc aat ggc gtg gag		720
Gln Trp Leu Asn Arg Arg	Ala Asn Ala Leu Leu Ala Asn Gly Val Glu		
225	230	235	240
ctg aga gat aac cag ctg gtg gtg cca tca	gag ggc ctg tac ctc atc		768
Leu Arg Asp Asn Gln Leu Val Val Pro Ser	Glu Gly Leu Tyr Leu Ile		
245	250	255	
tac tcc cag gtc ctc ttc aag ggc caa ggc tgc ccc tcc acc cat gtg			816
Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val			
260	265	270	
ctc ctc acc cac acc atc agc cgc atc gcc gtc tcc tac cag acc aag			864
Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys			
275	280	285	
gtc aac ctc ctc tct gcc atc aag agc ccc tgc cag agg gag acc cca			912
Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro			
290	295	300	
gag ggg gct gag gcc aag ccc tgg tat gag ccc atc tat ctg gga ggg			960
Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly			
305	310	315	320
gtc ttc cag ctg gag aag ggt gac cga ctc agc gct gag atc aat cgg			1008
Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg			
325	330	335	
ccc gac tat ctc gac ttt gcc gag tct ggg cag gtc tac ttt ggg atc			1056
Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile			
340	345	350	
att gcc ctg ggt ggc ggt tct ggt ggc ggt tct ggt ggc ggt tct ggt			1104
Ile Ala Leu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly			
355	360	365	
ggc gga tca tca tct tct cga acc ccg agt gac aag cct gta gcc cat			1152
Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His			
370	375	380	
gtt gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc			1200
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg			
385	390	395	400
cgg gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag			1248
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln			
405	410	415	
ctg gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc			1296
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu			
420	425	430	
ttc aag ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc			1344
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr			
435	440	445	
atc agc cgc atc gcc gtc tcc tac cag acc aag gtc aac ctc ctc tct			1392

TherapheresisSeq Listing.txt

Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 450 455 460

gcc atc aag agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc 1440
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 465 470 475 480

aag ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag 1488
 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 485 490 495

aag ggt gac cga ctc agc gct gag atc aat cggt ccc gac tat ctc gac 1536
 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 500 505 510

ttt gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg tga 1581
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 515 520 525

<210> 34

<211> 526

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scTNF peptide sequence

<400> 34

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala
 1 5 10 15

Ala Ala Asp Tyr Lys Asp Asp Asp Lys Glu Phe Gly Ser Ser Ser
 20 25 30

Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
 35 40 45

Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
 50 55 60

Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
 65 70 75 80

Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
 85 90 95

Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
 100 105 110

Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
 115 120 125

Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
 Page 27

TherapheresisSeq Listing.txt

130	135	140	
Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser			
145	150	155	160
Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln			
165	170	175	
Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Ser			
180	185	190	
Gly Gly Ser Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp			
195	200	205	
Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu			
210	215	220	
Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu			
225	230	235	240
Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile			
245	250	255	
Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val			
260	265	270	
Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys			
275	280	285	
Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro			
290	295	300	
Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly			
305	310	315	320
Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg			
325	330	335	
Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile			
340	345	350	
Ile Ala Leu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly			
355	360	365	
Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His			
370	375	380	

TherapheresisSeq Listing.txt

Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
385 390 395 400

Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
405 410 415

Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
420 425 430

Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
435 440 445

Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
450 455 460

Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
465 470 475 480

Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
485 490 495

Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
500 505 510

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
515 520 525

<210> 35

<211> 2253

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scFasL-AMAIze sequence

<220>

<221> CDS

<222> (1)..(2250)

<400> 35

atg gac tgg acc tgg cgc gtg ttt tgc ctg ctc gcc gtg gct cct ggg
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

48

gcc cac agc cag gta cag ctg gtg cag tct ggg gga ggc atg gta gag
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Met Val Glu
20 25 30

96

cct ggg ggg tcc ctt aga ctc tcc tgt gca gcc tct gga ttc act ttc
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

144

agt aat gcc tgg atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg

192

TherapheresisSeq Listing.txt

Ser	Asn	Ala	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
50				55					60							
gag	tgg	gtt	ggc	cgt	ata	aaa	agc	aaa	gct	ggt	ggt	ggg	aca	gca	gag	240
Glu	Trp	Val	Gly	Arg	Ile	Lys	Ser	Lys	Ala	Gly	Gly	Gly	Thr	Ala	Glu	
65					70				75				80			
tac	gct	gca	ccc	gtg	aaa	ggc	aga	ttc	acc	atc	tca	aga	gat	gat	tca	288
Tyr	Ala	Ala	Pro	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	
					85			90				95				
caa	aac	acg	ctg	tat	ctg	caa	atg	aac	agc	ctg	aaa	acc	gac	gac	aca	336
Gln	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Asp	Asp	Thr	
			100			105						110				
gcc	gtg	tat	tac	tgt	acc	aca	cat	gtc	tac	ggt	gcc	ccc	cgg	aac	tgg	384
Ala	Val	Tyr	Tyr	Cys	Thr	His	Val	Tyr	Gly	Ala	Pro	Arg	Asn	Trp		
			115			120				125						
ggc	cag	gga	tcc	ctg	gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	432
Gly	Gln	Gly	Ser	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	
			130			135				140						
aag	ctt	gaa	gaa	ggt	gaa	ttt	tca	gaa	gca	cgc	gtc	cag	tct	gtg	ttg	480
Lys	Leu	Glu	Glu	Gly	Glu	Phe	Ser	Glu	Ala	Arg	Val	Gln	Ser	Val	Leu	
	145				150				155			160				
act	cag	ccg	ccc	tca	gtg	tct	gcf	gcc	cca	gga	cag	aag	gtc	acc	atc	528
Thr	Gln	Pro	Pro	Ser	Val	Ser	Ala	Ala	Pro	Gly	Gln	Lys	Val	Thr	Ile	
				165			170					175				
tcc	tgc	tct	gga	agc	agc	tcc	aac	att	gga	aat	aat	tat	gtc	tcc	tgg	576
Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Asn	Asn	Tyr	Val	Ser	Trp	
			180			185						190				
tac	gtt	caa	ctc	cca	gga	aca	gcc	ccc	aaa	ctc	ctc	att	tat	gac	aat	624
Tyr	Val	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Asn	
			195			200						205				
aat	aag	cga	tcc	tca	gga	gtt	cct	gac	cga	ttc	tct	ggc	tcc	aag	tct	672
Asn	Lys	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	
			210			215					220					
ggc	acg	tca	gcc	acc	ctg	ggc	atc	acc	ggg	ctc	cag	act	ggg	gac	gag	720
Gly	Thr	Ser	Ala	Thr	Leu	Gly	Ile	Thr	Gly	Leu	Gln	Thr	Gly	Asp	Glu	
			225			230				235				240		
gcc	gat	tat	tac	tgc	gga	gca	tgg	gat	ggc	agc	ctg	cgt	gaa	gcf	gtg	768
Ala	Asp	Tyr	Tyr	Cys	Gly	Ala	Trp	Asp	Gly	Ser	Leu	Arg	Glu	Ala	Val	
				245			250						255			
ttc	ggc	gga	ggg	acc	aag	gtc	acc	gtc	cta	ggt	gcf	gcc	gca	gtt	gag	816
Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Ala	Ala	Ala	Ala	Val	
				260			265					270				
ctc	gag	gcf	gcc	gcf	gat	tac	aaa	gac	gat	gac	gat	aaa	gaa	ttc	acg	864
Leu	Glu	Ala	Ala	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Glu	Phe	Thr	
				275			280					285				
cgt	gaa	aaa	aag	gag	ctg	agg	aaa	gtg	gcc	cat	tta	aca	ggc	aag	tcc	912
Arg	Glu	Lys	Lys	Glu	Leu	Arg	Lys	Val	Ala	His	Leu	Thr	Gly	Lys	Ser	
			290			295					300					

TherapheresisSeq Listing.txt

aac tca agg tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val 305 310 315 320	960
ctg ctt tct gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu 325 330 335	1008
act ggg ctg tac ttt gta tat tcc aaa gta tac ttc cggttcaa tct aag Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser 340 345 350	1056
tgc aac aac ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys 355 360 365	1104
tat ccc cag gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys 370 375 380	1152
act act ggg cag atg tgg gcc cgc agc agc tac ctg ggg gca gtg ttc Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe 385 390 395 400	1200
aat ctt acc agt gct gat cat tta tat gtc aac gta tct gag ctc tct Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser 405 410 415	1248
ctg gtc aat ttt gag gaa tct cag acg ttt ttc ggc tta tat aag ctc Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu 420 425 430	1296
ggg ggc ggt tct ggt ggc ggt tct ggt ggc ggt tct ggt ggc gga tca Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser 435 440 445	1344
gaa aaa aag gag ctg agg aaa gtg gcc cat tta aca ggc aag tcc aac Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn 450 455 460	1392
tca agg tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc ctg Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu 465 470 475 480	1440
ctt tct gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa act Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr 485 490 495	1488
ggg ctg tac ttt gta tat tcc aaa gta tac ttc cggttcaa tct tgc Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys 500 505 510	1536
aac aac ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag tat Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr 515 520 525	1584
ccc cag gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc act Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr 530 535 540	1632
act ggg cag atg tgg gcc cgc agc agc tac ctg ggg gca gtg ttc aat Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn 545 550 555 560	1680

TherapheresisSeq Listing.txt

ctt acc agt gct gat cat tta tat gtc aac gta tct gag ctc tct ctg Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu 565 570 575	1728
gtc aat ttt gag gaa tct cag acg ttt ttc ggc tta tat aag ctc ggt Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly 580 585 590	1776
ggc ggt tct ggt ggc ggt tct ggt ggc ggt tct ggt ggc gga tcc gaa Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Glu 595 600 605	1824
aaa aag gag ctg agg aaa gtg gcc cat tta aca ggc aag tcc aac tca Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser 610 615 620	1872
agg tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc ctg ctt Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu 625 630 635 640	1920
tct gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa act ggg Ser Gly Val Lys Tyr Lys Gly Gly Leu Val Ile Asn Glu Thr Gly 645 650 655	1968
ctg tac ttt gta tat tcc aaa gta tac ttc cgg ggt caa tct tgc aac Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn 660 665 670	2016
aac ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag tat ccc Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro 675 680 685	2064
cag gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc act act Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr 690 695 700	2112
ggg cag atg tgg gcc cgc agc agc tac ctg ggg gca gtg ttc aat ctt Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu 705 710 715 720	2160
acc agt gct gat cat tta tat gtc aac gta tct gag ctc tct ctg gtc Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val 725 730 735	2208
aat ttt gag gaa tct cag acg ttt ttc ggc tta tat aag ctc tga Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu 740 745 750	2253

<210> 36
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scFasL-AMAIze peptide sequence
<400> 36

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

TherapheresisSeq Listing.txt

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu
65 70 75 80

Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Thr His Val Tyr Gly Ala Pro Arg Asn Trp
115 120 125

Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Ser Val Leu
145 150 155 160

Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile
165 170 175

Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp
180 185 190

Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn
195 200 205

Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
210 215 220

Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu
225 230 235 240

Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala Val
245 250 255

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Val Glu
260 265 270

TherapheresisSeq Listing.txt

Leu Glu Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Thr
275 280 285

Arg Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser
290 295 300

Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val
305 310 315 320

Leu Leu Ser Gly Val Lys Tyr Lys Gly Gly Leu Val Ile Asn Glu
325 330 335

Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser
340 345 350

Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys
355 360 365

Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys
370 375 380

Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe
385 390 395 400

Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser
405 410 415

Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
420 425 430

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
435 440 445

Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn
450 455 460

Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu
465 470 475 480

Leu Ser Gly Val Lys Tyr Lys Gly Gly Leu Val Ile Asn Glu Thr
485 490 495

Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys
500 505 510

Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr

TherapheresisSeq Listing.txt
515 520 525

Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr
530 535 540

Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn
545 550 555 560

Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu
565 570 575

Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly
580 585 590

Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Glu
595 600 605

Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser
610 615 620

Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu
625 630 635 640

Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly
645 650 655

Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn
660 665 670

Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro
675 680 685

Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr
690 695 700

Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu
705 710 715 720

Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val
725 730 735

Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
740 745 750

<210> 37
<211> 2646
<212> DNA
<213> Artificial sequence

TherapheresisSeq Listing.txt

<220>

<223> Description of Artificial Sequence: scTRAIL-AMAIze sequence

<220>

<221> CDS

<222> (1)...(2643)

<400> 37

atg gac tgg acc tgg cgc gtg ttt tgc ctg ctc gcc gtc gct cct ggg Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly	48
1 5 10 15	
gcc cac agc cag gta cag ctg gtg cag tct ggg gga ggc atg gta gag Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu	96
20 25 30	
cct ggg ggg tcc ctt aga ctc tcc tgt gca gcc tct gga ttc act ttc Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	144
35 40 45	
agt aat gcc tgg atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	192
50 55 60	
gag tgg gtt ggc cgt ata aaa agc aaa gct ggt ggt ggg aca gca gag Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu	240
65 70 75 80	
tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat tca Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser	288
85 90 95	
caa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gac gac aca Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr	336
100 105 110	
gcc gtg tat tac tgt acc aca cat gtc tac ggt gcc ccc cg aac tgg Ala Val Tyr Tyr Cys Thr Thr His Val Tyr Gly Ala Pro Arg Asn Trp	384
115 120 125	
ggc cag gga tcc ctg gtc acc gtc tcc tca gcc tcc acc aag ggc cca Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	432
130 135 140	
aag ctt gaa gaa ggt gaa ttt tca gaa gca cgc gta cag tct gtg ttg Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Ser Val Leu	480
145 150 155 160	
act cag ccg ccc tca gtg tct gcg gcc cca gga cag aag gtc acc atc Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile	528
165 170 175	
tcc tgc tct gga agc agc tcc aac att gga aat aat tat gtc tcc tgg Ser Cys Ser Gly Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp	576
180 185 190	
tac gtt caa ctc cca gga aca gcc ccc aaa ctc ctc att tat gac aat Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn	624
195 200 205	

TherapheresisSeq Listing.txt

aat aag cga ttc tca gga gtt cct gac cga ttc tct ggc tcc aag tct Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser 210 215 220	672
ggc acg tca gcc acc ctg ggc atc acc ggg ctc cag act ggg gac gag Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu 225 230 235 240	720
gcc gat tat tac tgc gga gca tgg gat ggc agc ctg cgt gaa gcg gta Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala Val 245 250 255	768
ttc ggc gga ggg acc aag gtc acc gtc cta ggt gcg gcc gca gtt gag Phe Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Val Glu 260 265 270	816
ctc gag gcg gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc gga Leu Glu Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly 275 280 285	864
acc tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile 290 295 300	912
tct ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile 305 310 315 320	960
act ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys 325 330 335	1008
aat gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg 340 345 350	1056
agt ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu 355 360 365	1104
gtc atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe 370 375 380	1152
cga ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met 385 390 395 400	1200
gtc caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu 405 410 415	1248
atg aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly 420 425 430	1296
ctc tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp 435 440 445	1344

TherapheresisSeq Listing.txt

aga att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat		1392
Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His		
450 455 460		
gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc ggt ggc ggt tct ggt		1440
Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Gly Ser Gly		
465 470 475 480		
ggc ggt tct ggt ggc ggt tct ggt ggc gga tca acc tct gag gaa acc		1488
Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Ser Glu Glu Thr		
485 490 495		
att tct aca gtt caa gaa aag caa caa aat att tct ccc cta gtg aga		1536
Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg		
500 505 510		
gaa aga ggt cct cag aga gta gca gct cac ata act ggg acc aga gga		1584
Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly		
515 520 525		
aga agc aac aca ttg tct tct cca aac tcc aag aat gaa aag gct ctg		1632
Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu		
530 535 540		
ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt ggg cat tca ttc		1680
Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe		
545 550 555 560		
ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc atc cat gaa aaa		1728
Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys		
565 570 575		
ggg ttt tac tac atc tat tcc caa aca tac ttt cga ttt cag gag gaa		1776
Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu		
580 585 590		
ata aaa gaa aac aca aag aac gac aaa caa atg gtc caa tat att tac		1824
Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr		
595 600 605		
aaa tac aca agt tat cct gac cct ata ttg ttg atg aaa agt gct aga		1872
Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg		
610 615 620		
aat agt tgt tgg tct aaa gat gca gaa tat gga ctc tat tcc atc tat		1920
Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr		
625 630 635 640		
caa ggg gga ata ttt gag ctt aag gaa aat gac aga att ttt gtt tct		1968
Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser		
645 650 655		
gta aca aat gag cac ttg ata gac atg gac cat gaa gcc agt ttt ttc		2016
Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe		
660 665 670		
ggg gcc ttt tta gtt ggc ggt ggc ggt tct ggt ggc ggt tct ggt ggc		2064
Gly Ala Phe Leu Val Gly Gly Ser Gly Gly Gly Ser Gly Gly		
675 680 685		
ggt tct ggt ggc gga tcc acc tct gag gaa acc att tct aca gtt caa		2112

TherapheresisSeq Listing.txt

Gly Ser Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln	
690 695 700	
gaa aag caa caa aat att tct ccc cta gtq aga gaa aga ggt cct cag	2160
Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln	
705 710 715 720	
aga gta gca gct cac ata act ggg acc aga gga aga agc aac aca ttg	2208
Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu	
725 730 735	
tct tct cca aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac	2256
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn	
740 745 750	
tcc tgg gaa tca tca agg agt ggg cat tca ttc ctg agc aac ttg cac	2304
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His	
755 760 765	
ttg agg aat ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc	2352
Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile	
770 775 780	
tat tcc caa aca tac ttt cga ttt cag gag gaa ata aaa gaa aac aca	2400
Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Ile Lys Glu Asn Thr	
785 790 795 800	
aag aac gac aaa caa atg gtc caa tat att tac aaa tac aca agt tat	2448
Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr	
805 810 815	
cct gac cct ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct	2496
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser	
820 825 830	
aaa gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga ata tt	2544
Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Ile Phe	
835 840 845	
gag ctt aag gaa aat gac aga att ttt gtt tct gta aca aat gag cac	2592
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His	
850 855 860	
ttg ata gac atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt	2640
Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val	
865 870 875 880	
ggc tga	2646
Gly	

<210> 38
<211> 881
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTRAIL-AMAIZE peptide sequence
<400> 38

TherapheresisSeq Listing.txt

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu
65 70 75 80

Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Thr His Val Tyr Gly Ala Pro Arg Asn Trp
115 120 125

Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Ser Val Leu
145 150 155 160

Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile
165 170 175

Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp
180 185 190

Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn
195 200 205

Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
210 215 220

Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu
225 230 235 240

Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala Val
245 250 255

TherapheresisSeq Listing.txt

Phe Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Val Glu
260 265 270

Leu Glu Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly
275 280 285

Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile
290 295 300

Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile
305 310 315 320

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
325 330 335

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
340 345 350

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
355 360 365

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
370 375 380

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
385 390 395 400

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
405 410 415

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
420 425 430

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
435 440 445

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
450 455 460

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Ser Gly
465 470 475 480

Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Ser Glu Glu Thr
485 490 495

Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg

TherapheresisSeq Listing.txt

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
515 520 525

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
530 535 540

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
545 550 555 560

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
565 570 575

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
580 585 590

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
595 600 605

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
610 615 620

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
625 630 635 640

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
645 650 655

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
660 665 670

Gly Ala Phe Leu Val Gly Gly Gly Ser Gly Gly Ser Gly Gly
675 680 685

Gly Ser Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln
690 695 700

Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
705 710 715 720

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
725 730 735

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
740 745 750

TherapheresisSeq Listing.txt

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
755 760 765

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
770 775 780

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
785 790 795 800

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
805 810 815

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
820 825 830

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
835 840 845

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
850 855 860

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
865 870 875 880

Gly

<210> 39
<211> 2358

<212> DNA

<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: scTNF-AMAIZE sequence

<220>

<221> CDS

<222> (1)..(2355)

<400> 39

atg gac tgg acc tgg cgc gtg ttt tgc ctg ctc gcc gtg gct cct ggg
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

48

gcc cac agc cag gta cag ctg gtg cag tct ggg gga ggc atg gta gag
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Met Val Glu
20 25 30

96

cct ggg ggg tcc ctt aga ctc tcc tgt gca gcc tct gga ttc act ttc
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

144

TherapheresisSeq Listing.txt

agt aat gcc tgg atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg	Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	192
50 55 60		
gag tgg gtt ggc cgt ata aaa agc aaa gct ggt ggt ggg aca gca gag	Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Thr Ala Glu	240
65 70 75 80		
tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat tca	Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser	288
85 90 95		
caa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gac gac aca	Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr	336
100 105 110		
gcc gtg tat tac tgt acc aca cat gtc tac ggt gcc ccc cgg aac tgg	Ala Val Tyr Tyr Cys Thr His Val Tyr Gly Ala Pro Arg Asn Trp	384
115 120 125		
ggc cag gga tcc ctg gtc acc gtc tcc tca gcc tcc acc aag ggc cca	Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	432
130 135 140		
aag ctt gaa gaa ggt gaa ttt tca gaa gca cgc gta cag tct gtg ttg	Lys Leu Glu Glu Gly Glu Ser Glu Ala Arg Val Gln Ser Val Leu	480
145 150 155 160		
act cag ccg ccc tca gtg tct gcg gcc cca gga cag aag gtc acc atc	Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile	528
165 170 175		
tcc tgc tct gga agc agc tcc aac att gga aat aat tat gtc tcc tgg	Ser Cys Ser Gly Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp	576
180 185 190		
tac gtt caa ctc cca gga aca gcc ccc aaa ctc ctc att tat gac aat	Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn	624
195 200 205		
aat aag cga ttc tca gga gtt cct gac cga ttc tct ggc tcc aag tct	Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser	672
210 215 220		
ggc acg tca gcc acc ctg ggc atc acc ggg ctc cag act ggg gac gag	Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu	720
225 230 235 240		
gcc gat tat tac tgc gga gca tgg gat ggc agc ctg cgt gaa gcg gta	Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala Val	768
245 250 255		
ttc ggc gga ggg acc aag gtc acc gtc cta ggt gcg gcc gca gtt gag	Phe Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Val Glu	816
260 265 270		
ctc gag gcg gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc gga	Leu Glu Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly	864
275 280 285		
tca tct tct cga acc ccg agt gac aag cct gta gcc cat gtt gta gca	Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala	912
290 295 300		

TherapheresisSeq Listing.txt

aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat		960
Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn		
305 310 315 320		
gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg		1008
Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val		
325 330 335 335		
cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc		1056
Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly		
340 345 350 350		
caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc		1104
Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg		
355 360 365 365		
atc gcc gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag		1152
Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys		
370 375 380 380		
agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg		1200
Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp		
385 390 395 400		
tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac		1248
Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp		
405 410 415 415		
cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag		1296
Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu		
420 425 430 430		
tct ggg cag gtc tac ttt ggg atc att gcc ctg ggt ggc ggt tct ggt		1344
Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly		
435 440 445 445		
ggc ggt tct ggt ggc ggt tct ggt ggc gga tca tca tct tct cga acc		1392
Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser Arg Thr		
450 455 460 460		
ccg agt gac aag cct gta gcc cat gtt gta gca aac cct caa gct gag		1440
Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu		
465 470 475 480		
ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc ctg gcc aat		1488
Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn		
485 490 495 495		
ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca gag ggc ctg		1536
Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu		
500 505 510 510		
tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc tgc ccc tcc		1584
Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser		
515 520 525 525		
acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc gtc tcc tac		1632
Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr		
530 535 540 540		
cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc tgc cag agg		1680
Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg		

TherapheresisSeq Listing.txt

545	550	555	560	
gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag ccc atc tat Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr 565	570	575	575	1728
ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc agc gct gag Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu 580	585	590		1776
atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg cag gtc tac Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr 595	600	605		1824
ttt ggg atc att gcc ctg ggt ggc ggt tct ggt ggc ggt tct ggt ggc Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Ser Gly Gly 610	615	620		1872
ggt tct ggt ggc gga tca tca tct tct cga acc ccg agt gac aag cct Gly Ser Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro 625	630	635	640	1920
gta gcc cat gtt gta gca aac cct caa gct gag ggg cag ctc cag tgg Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp 645	650	655		1968
ctg aac cgc cgg gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg 660	665	670		2016
gat aac cag ctg gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser 675	680	685		2064
cag gtc ctc ttc aag ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu 690	695	700		2112
acc cac acc atc agc cgc atc gcc gtc tcc tac cag acc aag gtc aac Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn 705	710	715	720	2160
ctc ctc tct gcc atc aag agc ccc tgc cag agg gag acc cca gag ggg Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly 725	730	735		2208
gct gag gcc aag ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe 740	745	750		2256
cag ctg gag aag ggt gac cga ctc agc gct gag atc aat cgg ccc gac Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp 755	760	765		2304
tat ctc gac ttt gcc gag tct ggg cag gtc tac ttt ggg atc att gcc Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala 770	775	780		2352
ctg tga Leu				2358
785				

TherapheresisSeq Listing.txt

<210> 40
<211> 785

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: TNF-AMAIZE peptide sequence

<400> 40

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu
65 70 75 80

Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Thr His Val Tyr Gly Ala Pro Arg Asn Trp
115 120 125

Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Ser Val Leu
145 150 155 160

Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile
165 170 175

Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp
180 185 190

Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn
195 200 205

Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
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TherapheresisSeq Listing.txt

210	215	220
Gly	Thr Ser Ala Thr Leu	Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu
225	230	235 240
Ala Asp Tyr Tyr Cys	Gly Ala Trp Asp	Gly Ser Leu Arg Glu Ala Val
245	250	255
Phe Gly Gly	Thr Lys Val Thr Val	Leu Gly Ala Ala Ala Val Glu
260	265	270
Leu Glu Ala Ala Ala Asp Tyr	Lys Asp Asp Asp Asp	Lys Glu Phe Gly
275	280	285
Ser Ser Ser Arg Thr Pro	Ser Asp Lys Pro Val	Ala His Val Val Ala
290	295	300
Asn Pro Gln Ala Glu	Gly Gln Leu Gln Trp	Leu Asn Arg Arg Ala Asn
305	310	315 320
Ala Leu Leu Ala Asn	Gly Val Glu Leu Arg	Asp Asn Gln Leu Val Val
325	330	335
Pro Ser Glu Gly	Leu Tyr Leu Ile	Tyr Ser Gln Val Leu Phe Lys Gly
340	345	350
Gln Gly Cys	Pro Ser Thr His Val	Leu Leu Thr His Thr Ile Ser Arg
355	360	365
Ile Ala Val Ser Tyr	Gln Thr Lys Val Asn Leu	Leu Ser Ala Ile Lys
370	375	380
Ser Pro Cys Gln Arg	Glu Thr Pro Glu Gly	Ala Glu Ala Lys Pro Trp
385	390	395 400
Tyr Glu Pro Ile Tyr	Leu Gly Gly Val	Phe Gln Leu Glu Lys Gly Asp
405	410	415
Arg Leu Ser Ala Glu	Ile Asn Arg Pro Asp Tyr	Leu Asp Phe Ala Glu
420	425	430
Ser Gly Gln Val	Tyr Phe Gly Ile	Ile Ala Leu Gly Gly Ser Gly
435	440	445
Gly Gly Ser Gly	Gly Ser Gly Gly Ser	Ser Ser Ser Arg Thr
450	455	460

TherapheresisSeq Listing.txt

Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu
465 470 475 480

Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn
485 490 495

Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu
500 505 510

Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser
515 520 525

Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr
530 535 540

Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg
545 550 555 560

Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr
565 570 575

Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
580 585 590

Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr
595 600 605

Phe Gly Ile Ile Ala Leu Gly Gly Ser Gly Gly Ser Gly Gly
610 615 620

Gly Ser Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro
625 630 635 640

Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp
645 650 655

Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg
660 665 670

Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
675 680 685

Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu
690 695 700

Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn
705 710 715 720

TherapheresisSeq Listing.txt

Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly
725 730 735

Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe
740 745 750

Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp
755 760 765

Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala
770 775 780

Leu
785

<210> 41
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide linker sequence

<400> 41

Gly Gly Gly Ser
1